

Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. - 79. (Canceled)

80. (Previously Presented) A polypeptide consisting essentially of:

a first interactor domain covalently bonded to a circularly permuted β -lactamase protein through an N-terminal breakpoint of the circularly permuted β -lactamase protein and a second interactor domain covalently bonded to the circularly permuted β -lactamase protein through a C-terminal breakpoint of the circularly permuted β -lactamase protein, wherein said circularly permuted β -lactamase protein is functionally reconstituted only upon binding of said first interactor domain and said second interactor domain to a single ligand.

81. - 83. (Canceled)

84. (Currently Amended) The polypeptide of claim 80, wherein said N-terminal break point and said C-terminal break point are within a solvent exposed loop between elements of secondary structure within the ~~enzyme~~ β -lactamase protein.

85. (Currently Amended) The polypeptide of claim 80, wherein said circularly permuted β -lactamase protein ~~is a β -lactamase protein that has been circularly permuted, said β -lactamase protein consisting~~ consists of amino acids 26 to 288 of the following sequence prior to circular permutation:

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly
26				30				35					40		
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu
			45				50					55			
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys

60 65 70
Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
75 80 85
Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
90 95 100 105
Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
110 115 120
Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
125 130 135
Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
140 145 150
Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
155 160 165
Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
170 175 180 185
Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
190 195 200
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
205 210 215
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
220 225 230
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
235 240 245
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
250 255 260 265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
270 275 280
Ala Ser Leu Ile Lys His Trp
285

(SEQ ID NO: 2);

wherein said N-terminal breakpoint and said C-terminal breakpoint are within 10 amino acids of an amide bond junction between two amino acids selected from the group consisting of asparagine 52 and serine 53, leucine 91 and glycine 92, glutamine 99 and asparagine 100, proline 174 and asparagine 175, glutamic acid 197 and leucine 198, lysine 215 and valine 216, alanine 227 and glycine 228, and glycine 253 and lysine 254.

86. (Previously Presented) The polypeptide of claim 85, wherein said two amino acids are selected from the group consisting of proline 174 and asparagine 175, glutamic acid 197 and leucine 198, lysine 215 and valine 216, alanine 227 and glycine 228, and glycine 253 and lysine 254.

87. (Previously Presented) The polypeptide of claim 85, wherein said two amino acids are glutamic acid 197 and leucine 198.

88. (Previously Presented) The polypeptide of claim 80, wherein said ligand is a protein ligand.

89. (Canceled)